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ON protein - nucleic search, using frame-plus-F2a model

Run on: January 16, 2003, 16:55:57 ; search time 440.224 Seconds  
330.553 Million cell updates/sec

Title: US-09-856-070-25  
Perfect score: 23

Sequence: 1 MRLQ \*

Scoring table: BLOSUM62

Xgapop 10.0 / Xapext 0.5  
Ygapop 10.0 / Yapext 0.5  
Fgapop 6.0 / Fapext 7.0  
Delop 6.0 / Delext 7.0

Searched: 2054640 seqs, 1451402878 res; dues

Total number of hits satisfied: 0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL="frame-plus-F2a model" DEFLATEP  
-Q/-Lrgn1.7/SRPL/-SPOOL/-SUSP/-GzRn1.14012504/-Lg844/-Lg1592  
-DB=genEmbl -QFMT=fastA -SUFFIX=seq -MINMATCH=0.1 -LwE=1.0 -LnPEX=0  
-UNITS=bins -START1=END-1 -MATPIX=bins62 -TRANS=human40 cod1 -LIST=45  
-DOALIGN=200 -THR=SCORE=prec -THR=MAX=100 -THR=MIN=0 -ALIGN=15 -MODE=DFAV  
-OUTfmt="pct" -NORMext="HEAPSIZE=500" -MAXLEN=0 -MAXLEN=200000000  
-USEH=US-09-856-070-25 -NC\_MMATCH=35 -NC\_SQRES=0 -NC\_HL=1 -NC\_HL=3  
-NO\_XIPXY -NO\_MMATCH=35 -LARGEQUERY -NFC\_SQRES=0 -WAIT=1 -LONG=10 -PTE=1-10  
-WARN TIMEOUT=10 -THREDDS=1 -XAPEXT=0 -XAPEXT=0 -FRAPOP=6 -FRAPEXT=7  
-YAPOP=10 -YAPEXT=0 5 -DELop=6 -DEFLext=7

Databases:

GenProtbl: \*  
1: qb\_ba: \*  
2: qb\_btg: \*  
3: qb\_ln: \*  
4: qb\_cm: \*  
5: qb\_ov: \*  
6: qb\_Pat: \*  
7: qb\_Ph: \*  
8: qb\_Pl: \*  
9: at\_pr: \*  
10: qb\_rc: \*  
11: ab\_sts: \*  
12: qb\_sy: \*  
13: qb\_un: \*  
14: qb\_vl: \*  
15: em\_ba: \*  
16: em\_tun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mj: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_Pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

Result No.	Score	Query Match length	DB ID	Description
1	24	10%	4	1.5.0.99
2	23	100.0	5.1	AX161287 Sequence
3	23	100.0	5.1	AX284883 Sequence
4	23	100.0	9.1	AX135207 Sequence
c	5	23	100.0	9.1
c	6	23	00.0	1.2.3
c	7	23	00.0	1.2.9
c	8	23	00.0	1.6.5.7.0.8
c	9	23	00.0	1.7.3
c	10	23	100.0	1.7.6
c	11	23	100.0	1.8.9
c	12	23	100.0	1.8.9
c	13	23	100.0	1.8.9
c	14	23	100.0	1.8.9
c	15	23	100.0	2.1.2
c	16	23	100.0	2.2.8
c	17	23	100.0	2.2.8
c	18	23	100.0	2.4.8
c	19	23	100.0	2.5.0
c	20	23	100.0	2.5.5
c	21	23	100.0	2.5.6
c	22	23	100.0	2.5.9
c	23	23	100.0	2.6.0
c	24	23	100.0	2.6.7
c	25	23	100.0	2.7.2
c	26	23	100.0	2.8.3
c	27	23	100.0	2.8.5
c	28	23	100.0	2.9.8
c	29	23	100.0	3.0.0
c	30	23	100.0	3.0.8
c	31	23	100.0	3.0.8
c	32	23	100.0	3.0.9
c	33	23	100.0	3.2.0
c	34	23	100.0	3.7.1
c	35	23	100.0	3.1.5
c	36	23	100.0	3.1.9
c	37	23	100.0	3.2.1
c	38	23	100.0	3.2.2
c	39	23	100.0	3.3.0
c	40	23	100.0	3.3.3
c	41	23	100.0	3.4.1
c	42	23	100.0	3.5.1
c	43	23	100.0	3.5.2
c	44	23	100.0	3.5.3
c	45	23	100.0	3.5.6

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	24	10%	4	1.5.0.99
2	23	100.0	5.1	AX161287 Sequence
3	23	100.0	5.1	AX284883 Sequence
4	23	100.0	9.1	AX135207 Sequence
c	5	23	100.0	9.1
c	6	23	00.0	1.2.3
c	7	23	00.0	1.2.9
c	8	23	00.0	1.6.5.7.0.8
c	9	23	00.0	1.7.3
c	10	23	100.0	1.7.6
c	11	23	100.0	1.8.9
c	12	23	100.0	1.8.9
c	13	23	100.0	1.8.9
c	14	23	100.0	1.8.9
c	15	23	100.0	2.1.2
c	16	23	100.0	2.2.8
c	17	23	100.0	2.2.8
c	18	23	100.0	2.4.8
c	19	23	100.0	2.5.0
c	20	23	100.0	2.5.5
c	21	23	100.0	2.5.6
c	22	23	100.0	2.5.9
c	23	23	100.0	2.6.0
c	24	23	100.0	2.6.7
c	25	23	100.0	2.7.2
c	26	23	100.0	2.8.3
c	27	23	100.0	2.8.5
c	28	23	100.0	2.9.8
c	29	23	100.0	3.0.0
c	30	23	100.0	3.0.8
c	31	23	100.0	3.0.8
c	32	23	100.0	3.0.9
c	33	23	100.0	3.2.0
c	34	23	100.0	3.7.1
c	35	23	100.0	3.1.5
c	36	23	100.0	3.1.9
c	37	23	100.0	3.2.1
c	38	23	100.0	3.2.2
c	39	23	100.0	3.3.0
c	40	23	100.0	3.3.3
c	41	23	100.0	3.4.1
c	42	23	100.0	3.5.1
c	43	23	100.0	3.5.2
c	44	23	100.0	3.5.3
c	45	23	100.0	3.5.6

### ALIGNMENTS

106509 Locus 106509 36 bp DNA linear PAT 02-MAR-1994  
 DEFINITION Sequence 13 from Patent WO 9002798.  
 ACCESSION 106509  
 VERSION 106509.1  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM unclassified.  
 REFERENCE 1 (bases 1 to 36).  
 AUTHORS Anderson, S., Bennett, W.F., Botstein, D., Higgins, D.L., Paoni, N.F., and Zoller, M.  
 TITLE TISSUE PLASMINOGEN ACTIVATOR HAVING ZYMOCENTIC OP FIBRIN SPECIFIC PROPERTIES.  
 JOURNAL Patent: WO 9002798-A 13 22 MAR 1990;  
 FEATURES Location/Qualifiers 1..46  
 source /organism="unknown"  
 BASE COUNT 9 a 7 c 8 q 12 t.  
 ORIGIN

RESULT 2  
 Locus AX161287 Sequence 4615 from Patent WO010521.  
 DEFINITION 51 bp DNA linear PAT 22-JUN-2001  
 VERSION AX161287  
 AUTHORS Stinkewitsch, R.A. and Leach, M.  
 KEYWORDS Nucleic acids containing single nucleotide polymorphisms and methods of use thereof.  
 JOURNAL Patent: WO 0140521-A 16/15 07-JUN-2001;  
 FEATURES Coragen Corporation (US) Location/Qualifiers 1..51  
 source /organism="Homo sapiens"  
 misc\_feature 26 /feature="of 2 allelic variants (Allele is either: mut1 or mut2)  
 BASE COUNT 11 a 15 c 14 q 11 t.  
 ORIGIN

Alignment Scores:  
 Pred. No.: 48.9  
 Score: 23.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 6

Length: 36  
 Matches: 5  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

RESULTS (1-5) x AX284883 (1-51)

QY 1 MetLeuArgLeuGln 5  
 YY 1 MetLeuArgLeuGln 5  
 DB 19 ATGCAGGGCTTCAG 33

RESULT 3  
 Locus AX284883 Sequence 688 from Patent WO0179556.  
 DEFINITION Sequence 688 from Patent WO0179556.  
 VERSION AX284883  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 91).  
 AUTHORS Lillie, J., Brown, J.L., Holt, A. and van Huffel, C.  
 TITLE Novel genes, compositions and methods for the identification, assessment, prevention, and therapy of human cancers  
 JOURNAL Patent: WO 0179556-A 6/8 25-OCT-2001;  
 FEATURES Location/Qualifiers 1..51  
 source /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 10 a 15 c 16 q 10 t.  
 ORIGIN

Alignment Scores:  
 Pred. No.: 70.1  
 Score: 23.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 6

Length: 51  
 Matches: 5  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

RESULTS (1-5) x AX284883 (1-51)

QY 1 MetLeuArgLeuGln 5  
 YY 1 MetLeuArgLeuGln 5  
 DB 19 ATGCAGGGCTTCAG 33

RESULT 4  
 Locus AX135207 Sequence 15 from Patent WO0133928.  
 DEFINITION 91 bp DNA linear PAT 29-MAY-2001  
 VERSION AX135207  
 AUTHORS Farr, S.  
 TITLE Methods of determining individual hypersensitivity to an agent  
 JOURNAL Patent: WO 0142715-A 15 10-MAY-2001;  
 FEATURES Location/Qualifiers 1..51  
 source /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 19 a 33 c 11 q 28 t.  
 ORIGIN

Alignment Scores:  
 Pred. No.: 70.1  
 Score: 23.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 6

Length: 91  
 Matches: 5  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

RESULTS (1-5) x AX135207 (1-51)

QY 1 MetLeuArgLeuGln 5  
 YY 1 MetLeuArgLeuGln 5  
 DB 19 ATGCAGGGCTTCAG 33



Pred. No.: 184 Length: 129  
Score: 2.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indexes: 0  
DB: 6 Caps: 0

RESULT 8  
G65968/C  
LOCUS 165968 bp DNA Linear STS 02-NOV-2001  
DEFINITION 806 Miscellaneous Y sequences Homo sapiens STS genomic sequence tagged site.  
ACCESSION G65968  
VERSION G65968.1 GI:15078019  
KEYWORDS Homo sapiens  
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ORGANISM

REFERENCE Tillord,C.A., Kuroda,Kawauchi,T., Skaltsky,H., Bozen,S., Brown,L.G., Rosenberg,M., McPherson,J.D., Wylie,K., Sekhon,M., Kucaba,T.A., Waterston,R.H., and Page,D.C.  
AUTHORS A physical map of the human Y chromosome  
TITLE Nature 409 (6822), 943-945 (2001)  
JOURNAL  
MEDLINE 21131744  
PUBMED 11237616  
COMMENT Contact: Tomoko Kawauchi  
Page Lab  
Whitehead Institute for Biomedical Research  
Room 423, 9 Cambridge Center, Cambridge, MA 02142, USA  
Email: kawauchi@w.mit.edu  
Primer A: TGTAGTTAGAGGAAGTCGG  
Primer B: AGGAAATAGGAGAACATTGCG  
STS size: 150  
PCR Profile:  
94°C 3:00 min  
45°C 94°C 1:00 sec  
45 x 60°C 1:00 min  
72°C 72°C 5:00 min  
Protocol:  
Temp/plate: 1 ul saturated bacterial culture (BACS) or 100  
nq DNA  
Primer: each 1 uM  
dNTPs: each 100 uM  
Taq Polymerase: 0.05 unit/  
Total Vol.: 15 ul or 20 ul  
Mineral Oil: 15 ul

Buffer: For 20ml of 10x Stock solution.  
Stock Reagent Volume Mixed  
1M KCl 10 ml  
1M Tris-HCl, pH 9.0 2 ml  
Triton X-100 200 ul  
2M MgCl2 150 ul  
H2O 7.65 ml.  
1.150  
Location/Qualifiers  
Source: /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="Miscellaneous Y sequences"  
/note="Human STS derived from miscellaneous Y sequences"  
/primer\_bind 1..150

primer\_bind complement(130..150) 43 q 43 t  
BASE COUNT 38 a 26 c 43 g 43 t  
ORIGIN

Alignment Scores:  
pred. No.: 213 Length: 150  
Score: 23.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indexes: 0  
DB: 11 Gaps: 0

US-09-856-070-25 (1-5) x G65968 (1-150)

QY 1 MetLeuArgLeuGln 5  
Rb: /db\_xref="GATGGATTAAGAG" 80

RESULT 9  
AX135383  
LOCUS AX135383 Sequence 191 from Patent WO0132928.  
DEFINITION Sequence 191 from Patent WO0132928.  
VERSION AX135383.1 GI:1427132  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 173)  
AUTHORS Parr,S.  
TITLE Methods of determining individual hypersensitivity to an agent  
JOURNAL Phase-I Molecular Toxicology Inc. (US)  
FEATURES Location/Qualifiers  
source /organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 59 a 25 c 40 q 49 t  
ORIGIN

Alignment Scores:  
pred. No.: 247 Length: 173  
Score: 23.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indexes: 0  
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135383 (1-173)

QY 1 MetLeuArgLeuGln 5  
Rb: /db\_xref="GATGGATTAAGAG" 81

RESULT 10  
ASA012135/C  
LOCUS ASA012135 Avena sativa mitochondrial cp-like tRNA-Ser (GUA) gene.  
DEFINITION Avena sativa mitochondrial cp-like tRNA-Ser (GUA) gene.  
VERSION A012135  
VERSION A012135.1 GI:112057053  
KEYWORDS transfer RNA-Ser; tRNA-Ser gene.  
SOURCE Mitochondrion Avena sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Kainaldi,G.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Kainaldi,G.  
TITLE Direct Submission

JOURNAL: Submitted (14-Oct-1998) Rainaldi G., Dipartimento di Biologia Molecolare, Universita' di Bari, via Cravenna 4, 70125 BARI, ITALY

FEATURES

source

Location/Qualifiers 1.

Organism="Aplysia californica"  
/db\_xref="taxon:4498"

gene

57..143  
/gene="tRNA-Ser (GGA)"

tRNA

57..143  
/gene="tRNA-Ser (GCA)"  
/product="tRNA-Ser"  
/evidence experimental

BASE COUNT 48 a 32 c 42 g 54 t

ORIGIN

Alignment Scores:

Pred. No.: 252 Length: 174

Score: 23.90 Matches: 5

Percent Similarity: 100.00% Conservation: 9

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-09-856-070-25 (1-5) x ASA012115 (1-176)

QY 1 MetileuArgLeuGln 5

Db 74 ATGTTGAGATTACG 60

RESULT 12

LOCUS G32522 Definition Human HOMO sapiens STS genomic, Sequence tagged site.

ACCESSION G32522

VERSION G32522.1

KEYWORDS STS.

SOURCE Homo sapiens.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 186)

AUTHORS Adams, M.D.

TITLE Human STS sequences

JOURNAL Unpublished (1996)

COMMENT

Contact: Mark Adams  
The Institute for Genomic Research  
9712 Meade, Rockville, MD 20850  
Email: mda@igs4.org  
Primer A: AGCCAGGTACAGCTATATGTC  
Primer B: AGGCAATGCCCTGTA  
STS size: 186  
PCR Profile: Denaturation: 96C 5min  
Anneal: 54C 30sec  
Extend: 72C 30sec  
Denature: 95C 30sec  
Primer A: AGCCAGGTACAGCTATATGTC  
Primer B: AGGCAATGCCCTGTA  
PCR Profile: Denaturation: 96C 5min  
Anneal: 54C 30sec  
Extend: 72C 30sec  
Denature: 95C 30sec  
Final Extend: 72C 5min  
Cycles: 30

Protocol: Glycerol: 25 μl  
GenomicDNA: 25 ng  
Primer: 0.43 μM each  
dNTPs: 230 μM each  
AmpliTaq: 0.5 units  
TaqStart Ab: 0.5 units  
Total Volume: 10 μl

Buffer: Tris HCl pH8.8: 100 mM  
KCl: 500 mM  
MgCl2: 20 mM  
Triton X-100: 1%  
Concentration: 10X

Prepared with primer pairs derived from IHC112360. GenBank Accession Numbers- R57895, R22414, 165722.

FEATURES

source

Location/Qualifiers 1.

Organism="Homo sapiens"  
/isolate="EWUM3/cha"  
/db\_xref="taxon:9606"  
/tissue-type="ewing's tumor"  
/note="derivative 11"  
/gene="FLJ\_1"

gene

misc\_feature

<1..103  
/gene="FLJ\_1"  
/note="FLJ\_1"  
/note="Y17293: location 44761..44863"  
106..180  
/gene="EWS"  
106..>180  
/gene="EWS"  
/note="Y08806: location 39688..39762"

BASE COUNT 55 a 22 c 44 g 59 t



PCR profile:  
 Presoak:  
 Denaturation:  
 Annealing: 56 degrees C  
 Polymerization:  
 PCR Cycles: 35  
 Thermal Cycler:  
 Protocol:  
 Template: 10 nq  
 Primer: each 5 pM  
 dNTPs: each 4 nM  
 Tag Polymerase: 0.025 units/ul  
 Total Vol: 20 ul

Buffer:

Mac12: 1.5 mM  
 KCl: 50 mM  
 Tris-HCl: 10 mM  
 pH: 9.3

FEATURES  
source  
derived from dbEST (genbank accession M63154).

Location/Qualifiers  
 1. .212  
 "organism="Homo sapiens"  
 /db\_xref="Taxon:9606"  
 /map="317.2 CR from top of Chr11 linkage group"  
 STS  
 12. .189  
 primer\_bind  
 12. .33  
 primer\_bind complement(.165, .189)  
 BASE COUNT 75 a 40 c 35 g 62 t  
 ORIGIN

Alignment Scores:

Pred. No.: 305 Length: 212  
 Score: 23.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

us-09-856-070-25 (1-5) x 32672 (1 212)

QY 1 MetIleArgLeuGln 5

DB 178 ATGTTGAGCTCTAG 164

Search completed: January 16, 2003, 19:05:57  
 Job time: 443.214 secs

